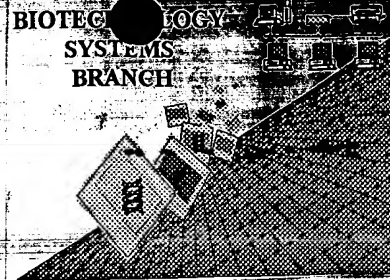


**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

Application Serial Number: 09/380,419
Source: 1655
Date Processed by STIC: 12/20/2000

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TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/380,419

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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J. Goldberg

1655

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,419

DATE: 12/20/2000
TIME: 15:02:54

Input Set : A:\MC4R.txt
Output Set: N:\CRF3\12202000\I380419.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Rothschild, Max F.
4 Kim, Kwan Suk
5 Emmett, Rebecca S.
7 <120> TITLE OF INVENTION: Melanocortin-4 Receptor Gene and Use as a Genetic
8 Marker for Fat Content, Weight Gain, and/or Feed
9 Consumption in Animals
11 <130> FILE REFERENCE: rothshcild mc4r2
13 <140> CURRENT APPLICATION NUMBER: 09/380,419
14 <141> CURRENT FILING DATE: 2000-07-24
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/16862
17 <151> PRIOR FILING DATE: 1999-07-26
19 <160> NUMBER OF SEQ ID NOS: 26
21 <170> SOFTWARE: PatentIn Ver. 2.0

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ERRORED SEQUENCES

23 <210> SEQ ID NO: 1
24 <211> LENGTH: 745
25 <212> TYPE: DNA
26 <213> ORGANISM: porcine
28 <220> FEATURE:
29 <221> NAME/KEY: variation
30 <222> LOCATION: (678)
31 <223> OTHER INFORMATION: G/A
33 <400> SEQUENCE: 1
34 acaagaatct gcatcaccr atgtactttt tcatctgtag cctggtctgt gctgatatgc 60
35 tggtagcggt ttccaatggg tcagaaacca ttgtcatcac cctattaaac agcacygaca 120
36 cggacgcaca gagtttcaca gtgaatttlg ataatgcat tgactcagtg atctgtagct 180
37 ccttaactcg ctcgaatttgc agcctgcttt cgattgcagt ggacaqtlat tttactatct 240
38 tttatgctct ccagtagcat aacattatga cagttlaagc ggttggaaac atcatcagtt 300
39 gtaactgggg agtetgcaag gtgtcgggtg ttttgttcat catttactca gatagcagtg 360
40 ctgttattat ctgctcatal accgtgttct taccatgct ggcctcatal gcttctctct 420
41 atgtccacat gtctcctatg gccagactcc acattaaagc gatcgccgtc ctcccaaggc 480
42 ctggcaccat ccgccaaggt gcccaacatga agggggccat taccctgacc atcttgatty 540
43 gggctcttlt ggtctgctgg gcccccttct tccctcactt aatattctat atctcctgcc 600
44 cccagaatcc atactgtgtg tgcctcatgt ctcactttaa ttgtatctc atcctgatca 660
45 tgtgtaatc catcatcgt cccctgattt atgcaactcc gagccaagaa ctgaggaaaa 720
E--> 46 ccttcaaaga gatcatctgt tgetat 746

746 shown

Per Sequence Rules, use "r" to represent
g or a; "g" can
only represent
itself

see next pages for more errors

09/380,419 2

<210> 3
<211> 311
<212> PRT
<213> Homo sapiens

see p.3

<400> 3
Gln Leu Phe Val Ser Pro Glu Val Phe Val Thr Leu Gly Val Ile Ser
1 5 10 15
Leu Leu Glu Asn Ile Leu Val Ile Val Ala Ile Ala Lys Asn Lys Asn
20 25 30
Leu His Ser Pro Met Tyr Phe Phe Ile Cys Ser Leu Ala Val Ala Asp
35 40 45
Met Leu Val Ser Val Ser Asn Gly Ser Glu Thr Ile Ile Ile Thr Leu
50 55 60
Leu Asn Ser Thr Asp Thr Asp Ala Gln Ser Phe Thr Val Asn Ile Asp
65 70 75 80
Asn Val Ile Asp Ser Val Ile Cys Ser Ser Leu Leu Ala Ser Ile Cys
85 90 95
Ser Leu Leu Ser Ile Ala Val Asp Arg Tyr Phe Thr Ile Phe Tyr Ala
100 105 110
Leu Gln Tyr His Asn Ile Met Thr Val Lys Arg Val Gly Ile Ser Ile
115 120 125
Ser Cys Ile Trp Ala Ala Cys Thr Val Ser Gly Ile Leu Phe Ile Ile
130 135 140
Tyr Ser Asp Ser Ser Ala Val Ile Ile Cys Leu Ile Thr Met Phe Phe
145 150 155 160
Thr Met Leu Ala Leu Met Ala Ser Leu Tyr Val His Met Phe Leu Met
165 170 175
Ala Arg Leu His Ile Lys Arg Ile Ala Val Leu Pro Gly Thr Gly Ala
180 185 190
Ile Arg Gln Gly Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu
195 200 205
Ile Gly Val Phe Val Val Cys Trp Ala Pro Phe Phe Leu His Leu Ile
210 215 220
Phe Tyr Ile Ser Cys Pro Gln Asn Pro Tyr Cys Val Cys Phe Met Ser
225 230 235 240
His Phe Asn Leu Tyr Leu Ile Leu Ile Met Cys Asn Ser Ile Ile Asp
245 250 255
Pro Leu Ile Tyr Ala Leu Arg Ser Gln Glu Leu Arg Lys Thr Phe Lys
260 265 270

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09/380,419 3

Glu Ile Ile Cys Cys Tyr Pro Leu Gly Gly Leu Cys Asp Leu Ser Ser
275 280 285

Arg Tyr Ala Pro Pro Glu Asn Asp Ile Xaa Val Ile Cys Asn Phe Ile
290 295 300

Asp Glu Asn Thr Ile Ala Leu
305 310

See Item 10 on Enol
Summary Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/380,419

DATE: 12/20/2000

TIME: 15:02:55

Input Set : A:\MC4R.txt

Output Set: N:\CRF3\12202000\I380419.raw

L:46 M:252 E: No. of Seq. differs, <211>LENGTH:Input:745 Found:746 SEQ:1
L:129 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:129 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:129 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:129 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:129 M:340 W: (46) "a" or "Xaa" used: Feature required, for SEQ ID#:3